

SEQUENCE LISTING

<110> Helix Research Institute

<120> FULL LENGTH cDNA CLONES AND PROTEINS ENCODED THEREBY

<130> H1-108PCT

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<150> JP 1999-209817

<151> 1999-07-23

<150> US 60/159,528

<151> 1999-10-18

<160> 12

<170> PatentIn Ver. 2.0

<210> 1

<211> 1246

<212> DNA

<213> Homo. sapiens...

<220>

<221> CDS

<222> (264)..(1151)

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ggctcctagg gttcgggacg gtacgcacca gccaccttcg cgccgaaggc ggtagggcgc 180

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cacggagagg aaccgctcta ggcacgtaag gcctcgtgag gttgcgtcgc gcgcggagca 240

ctctgggact tgtagttctg gag atg gag cga gct gtg ccg ctc gcg gtg cct 293

Met Glu Arg Ala Val Pro Leu Ala Val Pro

1

5

10

ctg ggt cag aca gag gtg ttc cag gcc ttg cag cgg ctc cat atg acc 341

Leu Gly Gln Thr Glu Val Phe Gln Ala Leu Gln Arg Leu His Met Thr

15

20

25

atc ttc tcc cag agc gtc tca cca tgt ggg aag ttt ctg gcg gct ggc 389

Ile Phe Ser Gln Ser Val Ser Pro Cys Gly Lys Phe Leu Ala Ala Gly

30

35

40

aac aat tac ggg cag att gcc atc ttc agc ttg tcc tct gct ttg agc 437

Asn Asn Tyr Gly Gln Ile Ala Ile Phe Ser Leu Ser Ser Ala Leu Ser

45

50

55

tca gaa gcc aaa gag gaa agt aag aag ccg gtg gtg act ttc caa gcc 485

Ser Glu Ala Lys Glu Glu Ser Lys Lys Pro Val Val Thr Phe Gln Ala

60

65

70

cat gat ggg ccc gtc tat agc atg gtt tcc acc gat cga cat ctg ctt 533

His Asp Gly Pro Val Tyr Ser Met Val Ser Thr Asp Arg His Leu Leu

75

80

85

90

agt gct ggg gat ggg gag gag aag gcc tgg ctt tgg gcg gag atg ctc 581

Ser Ala Gly Asp Gly Glu Glu Lys Ala Trp Leu Trp Ala Glu Met Leu

95

100

105

aag aag ggc tgt aag gag ctg tgg cgt cgt cag cct cca tac agg acc 629

Lys Lys Gly Cys Lys Glu Leu Trp Arg Arg Gln Pro Pro Tyr Arg Thr

110

115

120

agc ctg gaa gtg cct gag atc aac gct ttg ctg ctg gtc ccc aag gag 677

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Ser Leu Glu Val Pro Glu Ile Asn Ala Leu Leu Leu Val Pro Lys Glu
 125 130 135

aat tcc ctc atc ctg gct ggg gga gac tgt cag ttg cac act atg gac 725
 Asn Ser Leu Ile Leu Ala Gly Gly Asp Cys Gln Leu His Thr Met Asp
 140 145 150

ctt gaa act ggg act ttc acg agg gtc ctc cgg ggc cac aca gac tac 773
 Leu Glu Thr Gly Thr Phe Thr Arg Val Leu Arg Gly His Thr Asp Tyr
 155 160 165 170

atc cac tgc ctg gca ctg cgg gaa agg agc cca gag gtg ctg tca ggt 821
 Ile His Cys Leu Ala Leu Arg Glu Arg Ser Pro Glu Val Leu Ser Gly
 175 180 185

ggc gag gat gga gct gtt cga ctt tgg gac ctg cgc aca gcc aag gag 869
 Gly Glu Asp Gly Ala Val Arg Leu Trp Asp Leu Arg Thr Ala Lys Glu
 190 195 200

gtc cag acg atc gag gtc tat aag cac gag gag tgc tcg agg ccc cac 917
 Val Gln Thr Ile Glu Val Tyr Lys His Glu Glu Cys Ser Arg Pro His
 205 210 215

aat ggg cgc tgg att gga tgt ttg gca act gat tcc gac tgg atg gtc 965
 Asn Gly Arg Trp Ile Gly Cys Leu Ala Thr Asp Ser Asp Trp Met Val
 220 225 230

tgt gga ggg ggc cca gcc ctc acc ctc tgg cac ctc cga tcc tcc aca 1013
 Cys Gly Gly Gly Pro Ala Leu Thr Leu Trp His Leu Arg Ser Ser Thr
 235 240 245 250

ccc acc acc atc ttc ccc atc cgg gcg cca cag aag cac gtc acc ttc 1061
 Pro Thr Thr Ile Phe Pro Ile Arg Ala Pro Gln Lys His Val Thr Phe
 255 260 265

tac cag gac ctg gtc ctg aca gct gca ggc aac agc tgc cgg gtg gat 1109

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Tyr Gln Asp Leu Val Leu Thr Ala Ala Gly Asn Ser Cys Arg Val Asp
270 275 280

gtc ttc acc aac ctg ggt tac cga gcc ttc tcc ctg tcc ttc 1151
Val Phe Thr Asn Leu Gly Tyr Arg Ala Phe Ser Leu Ser Phe
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<211> 296

<212> PRT

<213> Homo sapiens

<400> 2

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20 25 30

Ser Pro Cys Gly Lys Phe Leu Ala Ala Gly Asn Asn Tyr Gly Gln Ile
35 40 45

Ala Ile Phe Ser Leu Ser Ser Ala Leu Ser Ser Glu Ala Lys Glu Glu
50 55 60

Ser Lys Lys Pro Val Val Thr Phe Gln Ala His Asp Gly Pro Val Tyr
65 70 75 80

Ser Met Val Ser Thr Asp Arg His Leu Leu Ser Ala Gly Asp Gly Glu
85 90 95

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Glu Lys Ala Trp Leu Trp Ala Glu Met Leu Lys Lys Gly Cys Lys Glu
 100 105 110

Leu Trp Arg Arg Gln Pro Pro Tyr Arg Thr Ser Leu Glu Val Pro Glu
 115 120 125

Ile Asn Ala Leu Leu Leu Val Pro Lys Glu Asn Ser Leu Ile Leu Ala
 130 135 140

Gly Gly Asp Cys Gln Leu His Thr Met Asp Leu Glu Thr Gly Thr Phe
 145 150 155 160

Thr Arg Val Leu Arg Gly His Thr Asp Tyr Ile His Cys Leu Ala Leu
 165 170 175

Arg Glu Arg Ser Pro Glu Val Leu Ser Gly Gly Glu Asp Gly Ala Val
 180 185 190

Arg Leu Trp Asp Leu Arg Thr Ala Lys Glu Val Gln Thr Ile Glu Val
 195 200 205

Tyr Lys His Glu Glu Cys Ser Arg Pro His Asn Gly Arg Trp Ile Gly
 210 215 220

Cys Leu Ala Thr Asp Ser Asp Trp Met Val Cys Gly Gly Gly Pro Ala
 225 230 235 240

Leu Thr Leu Trp His Leu Arg Ser Ser Thr Pro Thr Thr Ile Phe Pro
 245 250 255

Ile Arg Ala Pro Gln Lys His Val Thr Phe Tyr Gln Asp Leu Val Leu
 260 265 270

Thr Ala Ala Gly Asn Ser Cys Arg Val Asp Val Phe Thr Asn Leu Gly
 275 280 285

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Tyr Arg Ala Phe Ser Leu Ser Phe
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<212> DNA

<213> Homo sapiens

<220>

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<222> (659)..(1465)

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tccccccatc cgcgggcgcg aatgggtccg gtcgcgtccg cagtgtctgt ggctgtctcc 180
tggttgctgg gtgcaaagt ctgggttctg ggtttctgga ttcgcgggcc gttcacacgt 240
agcctgtgcc ggctcctcgg gtgagtcctt ccgcgcgcgg tgccccggga cggcctaggc 300
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gggtccctga ggatccgat gcctacgagc caagatgctc agctttatag gtgtgacct 480
cacatgtgac ttcacctcag ttttgtgatc cgtaaaatgg acaaattcga agctacttca 540
cagtgtgtt gagaggatta aatgaaacaa tgcttgtaaa gctctttgca ggaggagacc 600
tcggaagcag ggctggccg gcagagcaca cctgtgtgtc ccagggacca caggcagc 658

7/27

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Met Lys Thr Pro Val Glu Leu Ala Val Ser Gly Met Gln Thr Leu Gly	
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Leu Gln His Arg Cys Arg Gly Gly Tyr Arg Val Lys Ala Arg Thr Ser	
20 25 30	
tat gtg gat gag act ctg ttt ggc agc cca gca ggc acc cgg cct acc	802
Tyr Val Asp Glu Thr Leu Phe Gly Ser Pro Ala Gly Thr Arg Pro Thr	
35 40 45	
cca ccg gac ttc gat ccg ccc tgg gtg gag aag gct aac aga acc aga	850
Pro Pro Asp Phe Asp Pro Pro Trp Val Glu Lys Ala Asn Arg Thr Arg	
50 55 60	
ggc gtg ggc aag gag gca tgc aag gcc ttg ggg gca aag ggg agc tgt	898
Gly Val Gly Lys Glu Ala Ser Lys Ala Leu Gly Ala Lys Gly Ser Cys	
65 70 75 80	
gag acc acc ccc tca agg ggc agc acc ccc acc ctc aca cca agg aag	946
Glu Thr Thr Pro Ser Arg Gly Ser Thr Pro Thr Leu Thr Pro Arg Lys	
85 90 95	
aag aac aaa tac aga ccc atc age cac acc ccg tct tac tgt gat gag	994
Lys Asn Lys Tyr Arg Pro Ile Ser His Thr Pro Ser Tyr Cys Asp Glu	
100 105 110	
tgc ctg ttt ggc tcc cga tct gaa ggc gcc agc ttc ggg gcc ccg cgg	1042
Ser Leu Phe Gly Ser Arg Ser Glu Gly Ala Ser Phe Gly Ala Pro Arg	
115 120 125	
atg gcg aag ggg gat gcc gca aag ctc cgt gct ctc ttg tgg acg cca	1090
Met Ala Lys Gly Asp Ala Ala Lys Leu Arg Ala Leu Leu Trp Thr Pro	
130 135 140	

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cca cct acc ccc agg ggt agc cac tcg ccc cgc ccc agg gag gca cca	1138
Pro Pro Thr Pro Arg Gly Ser His Ser Pro Arg Pro Arg Glu Ala Pro	
145 150 155 160	
ctg cga gcc att cac cca gct ggt ccc tcc aag aca gag ccg ggg cca	1186
Leu Arg Ala Ile His Pro Ala Gly Pro Ser Lys Thr Glu Pro Gly Pro	
165 170 175	
gcg gca gac tcc cag aag tta tct atg ggt ggg tta cac tct tca cgc	1234
Ala Ala Asp Ser Gln Lys Leu Ser Met Gly Gly Leu His Ser Ser Arg	
180 185 190	
ccc ctg aag cgg gga ctt tcc cat tcc ctc acc cac ctg aat gtc ccc	1282
Pro Leu Lys Arg Gly Leu Ser His Ser Leu Thr His Leu Asn Val Pro	
195 200 205	
agc act ggt cat cca gcc acc agt gcc ccc cac aca aat ggg cct cag	1330
Ser Thr Gly His Pro Ala Thr Ser Ala Pro His Thr Asn Gly Pro Gln	
210 215 220	
gat ctc agg cct tcc acg tca ggg gtg acc ttc cgg agc ccc ctg gtg	1378
Asp Leu Arg Pro Ser Thr Ser Gly Val Thr Phe Arg Ser Pro Leu Val	
225 230 235 240	
act tcc agg gct cgc tca gtt agc att tca gtg cca tct acc cca cga	1426
Thr Ser Arg Ala Arg Ser Val Ser Ile Ser Val Pro Ser Thr Pro Arg	
245 250 255	
cga ggt ggg gcc acc cag aaa cca aag ccc cct tgg aaa tgatactctt	1475
Arg Gly Gly Ala Thr Gln Lys Pro Lys Pro Pro Trp Lys	
260 265	
tcatacagggt tgcctatggg gccacggcga caggtatggc cccttgccag ggtaggagga	1535
cattcatcac ccagggaacc ccaggtatta aagaagcccc tgtgggggca gacagacata	1595

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gcaggggtgg gcagtgcctc cctttatcct gacaatctct agtcgattct tgcctttttc 1655
 tcccgattgc ggatttgggg gccacctcta agatgcctct ctccagccct gtctcaacca 1715
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<210> 4

<211> 269

<212> PRT

<213> Homo sapiens

<400> 4

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			20					25					30		
Tyr	Val	Asp	Glu	Thr	Leu	Phe	Gly	Ser	Pro	Ala	Gly	Thr	Arg	Pro	Thr
		35					40					45			
Pro	Pro	Asp	Phe	Asp	Pro	Pro	Trp	Val	Glu	Lys	Ala	Asn	Arg	Thr	Arg
		50				55					60				
Gly	Val	Gly	Lys	Glu	Ala	Ser	Lys	Ala	Leu	Gly	Ala	Lys	Gly	Ser	Cys
65				70					75					80	
Glu	Thr	Thr	Pro	Ser	Arg	Gly	Ser	Thr	Pro	Thr	Leu	Thr	Pro	Arg	Lys
			85					90					95		
Lys	Asn	Lys	Tyr	Arg	Pro	Ile	Ser	His	Thr	Pro	Ser	Tyr	Cys	Asp	Glu
			100					105					110		

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Ser Leu Phe Gly Ser Arg Ser Glu Gly Ala Ser Phe Gly Ala Pro Arg
 115 120 125

Met Ala Lys Gly Asp Ala Ala Lys Leu Arg Ala Leu Leu Trp Thr Pro
 130 135 140

Pro Pro Thr Pro Arg Gly Ser His Ser Pro Arg Pro Arg Glu Ala Pro
 145 150 155 160

Leu Arg Ala Ile His Pro Ala Gly Pro Ser Lys Thr Glu Pro Gly Pro
 165 170 175

Ala Ala Asp Ser Gln Lys Leu Ser Met Gly Gly Leu His Ser Ser Arg
 180 185 190

Pro Leu Lys Arg Gly Leu Ser His Ser Leu Thr His Leu Asn Val Pro
 195 200 205

Ser Thr Gly His Pro Ala Thr Ser Ala Pro His Thr Asn Gly Pro Gln
 210 215 220

Asp Leu Arg Pro Ser Thr Ser Gly Val Thr Phe Arg Ser Pro Leu Val
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Arg Gly Gly Ala Thr Gln Lys Pro Lys Pro Pro Trp Lys
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<210> 5

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<212> DNA

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<220>

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<222> (183)..(2417)

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tccacaatct gggactcctc accaagccgg gtactctcct gcccaccgat aggaacaact 180

cc atg tgt acc acc atg cga gat aaa gtg ttt gga aat tac att cct 227

Met Cys Thr Thr Met Arg Asp Lys Val Phe Gly Asn Tyr Ile Pro

1

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gtg cct gct act gac tgt atg gct gtt tca act ttc tgg att gct cat 275

Val Pro Ala Thr Asp Cys Met Ala Val Ser Thr Phe Trp Ile Ala His

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25

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ccc aac aat aat ctg att aat aat gca gct gca ggc tca cag gat gct 323

Pro Asn Asn Asn Leu Ile Asn Asn Ala Ala Ala Gly Ser Gln Asp Ala

35

40

45

gga ata tgg tat tta ttc cac aag gaa cca act ggg gaa tcc agt gga 371

Gly Ile Trp Tyr Leu Phe His Lys Glu Pro Thr Gly Glu Ser Ser Gly

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55

60

ttg cag ctc ttg gca aaa cca gaa ctc act cca ttg ggt ata ttt tat 419

Leu Gln Leu Leu Ala Lys Pro Glu Leu Thr Pro Leu Gly Ile Phe Tyr

65

70

75

aac aac agg gtc cat tca aat ttt aag gct ggc tta ttt att gac aaa 467

Asn Asn Arg Val His Ser Asn Phe Lys Ala Gly Leu Phe Ile Asp Lys

80

85

90

95

ggg gtc aaa aca acc aac tct agt gct gct gac cca agg gaa tac ctc 515

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Gly Val Lys Thr Thr Asn Ser Ser Ala Ala Asp Pro Arg Glu Tyr Leu	
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tgt ttg gac aat agt gca aga ttt cga cct cat cag gat gca aac ccc	563
Cys Leu Asp Asn Ser Ala Arg Phe Arg Pro His Gln Asp Ala Asn Pro	
115	120 125
gaa aaa cca cgt gtt gct gct cta att gac agg ctc att gct ttt aaa	611
Glu Lys Pro Arg Val Ala Ala Leu Ile Asp Arg Leu Ile Ala Phe Lys	
130	135 140
aat aat gat aat gga gct tgg gtc aga gga gga gat att atc gtt caa	659
Asn Asn Asp Asn Gly Ala Trp Val Arg Gly Gly Asp Ile Ile Val Gln	
145	150 155
aat tca gca ttt gca gat aat gga ata gga ctg acc ttt gcc agt gat	707
Asn Ser Ala Phe Ala Asp Asn Gly Ile Gly Leu Thr Phe Ala Ser Asp	
160	165 170 175
gga agc ttc cca agt gat gaa ggt tcc agc caa gag gta tct gaa tct	755
Gly Ser Phe Pro Ser Asp Glu Gly Ser Ser Gln Glu Val Ser Glu Ser	
180	185 190
ctc ttt gtt ggg gag agc agg aat tac ggc ttt cag ggt ggt cag aac	803
Leu Phe Val Gly Glu Ser Arg Asn Tyr Gly Phe Gln Gly Gly Gln Asn	
195	200 205
aag tat gta ggc act gga gga ata gac cag aag cct cga aca tta ccc	851
Lys Tyr Val Gly Thr Gly Gly Ile Asp Gln Lys Pro Arg Thr Leu Pro	
210	215 220
agg aac agg acg ttc cca att aga ggc ttt cag att tat gat ggg ccc	899
Arg Asn Arg Thr Phe Pro Ile Arg Gly Phe Gln Ile Tyr Asp Gly Pro	
225	230 235
att cat ctc aca agg agc act ttc aaa aaa tat gtg cca act cca gat	947

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Ile His Leu Thr Arg Ser Thr Phe Lys Lys Tyr Val Pro Thr Pro Asp	
240	245 250 255
agg tac agc agt gca att ggc ttc ctc atg aag aat tcc tgg cag ata 995	
Arg Tyr Ser Ser Ala Ile Gly Phe Leu Met Lys Asn Ser Trp Gln Ile	
260	265 270
acc ccc agg aat aat atc tcc ctc gtg aag ttt ggt cca cat gtc tct 1043	
Thr Pro Arg Asn Asn Ile Ser Leu Val Lys Phe Gly Pro His Val Ser	
275	280 285
ctg aat gtc ttt ttt gga aag cct ggt ccc tgg ttt gaa gat tgt gag 1091	
Leu Asn Val Phe Phe Gly Lys Pro Gly Pro Trp Phe Glu Asp Cys Glu	
290	295 300
atg gat ggt gat aag aac tcc ata ttc cat gac att gat ggc tct gtg 1139	
Met Asp Gly Asp Lys Asn Ser Ile Phe His Asp Ile Asp Gly Ser Val	
305	310 315
aca gga tac aag gat gct tat gtg gga aga atg gac aac tac ctg atc 1187	
Thr Gly Tyr Lys Asp Ala Tyr Val Gly Arg Met Asp Asn Tyr Leu Ile	
320	325 330 335
cgc cat cca agc tgt gta aat gtg tct aag tgg aat gca gtg atc tgc 1235	
Arg His Pro Ser Cys Val Asn Val Ser Lys Trp Asn Ala Val Ile Cys	
340	345 350
agt ggg acc tat gca cag gtc tat gta cag aca tgg agc act cag aat 1283	
Ser Gly Thr Tyr Ala Gln Val Tyr Val Gln Thr Trp Ser Thr Gln Asn	
355	360 365
ctt tct atg acc att aca cga gat gag tat ccg tcc aac cct atg gtg 1331	
Leu Ser Met Thr Ile Thr Arg Asp Glu Tyr Pro Ser Asn Pro Met Val	
370	375 380
ctc cga ggt att aat cag aag gct gcc ttt cca cag tac cag cct gtc 1379	

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Leu	Arg	Gly	Ile	Asn	Gln	Lys	Ala	Ala	Phe	Pro	Gln	Tyr	Gln	Pro	Val		
385						390					395						
gtc atg ctg gag aag ggt tat acc atc cac tgg aat ggg ccg gca cca 1427																	
Val	Met	Leu	Glu	Lys	Gly	Tyr	Thr	Ile	His	Trp	Asn	Gly	Pro	Ala	Pro		
400					405					410				415			
cgg act aca ttt cta tac ctc gtc aac ttc aac aag aat gac tgg att 1475																	
Arg	Thr	Thr	Phe	Leu	Tyr	Leu	Val	Asn	Phe	Asn	Lys	Asn	Asp	Trp	Ile		
				420					425					430			
cga gtt ggc ctt tgc tat cca tca aac aca agt ttt caa gtt acc ttt 1523																	
Arg	Val	Gly	Leu	Cys	Tyr	Pro	Ser	Asn	Thr	Ser	Phe	Gln	Val	Thr	Phe		
			435					440					445				
ggc tat ttg cag cgg cag aat ggc tca tta tcc aaa atc gaa gaa tat 1571																	
Gly	Tyr	Leu	Gln	Arg	Gln	Asn	Gly	Ser	Leu	Ser	Lys	Ile	Glu	Glu	Tyr		
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aaa ttc tat ttt gac tcc agc acg ggg tta ctg ttt ttg tat ctc aaa 1667																	
Lys	Phe	Tyr	Phe	Asp	Ser	Ser	Thr	Gly	Leu	Leu	Phe	Leu	Tyr	Leu	Lys		
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gcc aaa agc cac agg cat ggc cac agt tac tgt tca tct cag gga tgt 1715																	
Ala	Lys	Ser	His	Arg	His	Gly	His	Ser	Tyr	Cys	Ser	Ser	Gln	Gly	Cys		
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gaa aga gtc aag atc caa gca gcc aca gac tca aag gac atc agt aac 1763																	
Glu	Arg	Val	Lys	Ile	Gln	Ala	Ala	Thr	Asp	Ser	Lys	Asp	Ile	Ser	Asn		
			515					520					525				
tgc atg gcc aaa gca tac cca cag tac tac aga aag ccg tca gtg gtc 1811																	

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Cys Met Ala Lys Ala Tyr Pro Gln Tyr Tyr Arg Lys Pro Ser Val Val
 530 535 540

aag cgg atg ccg gcc atg ctc act gga ctc tgt caa ggc tgt ggc act 1859
 Lys Arg Met Pro Ala Met Leu Thr Gly Leu Cys Gln Gly Cys Gly Thr
 545 550 555

cgg cag gtg gtg ttt act agt gat cct cat aaa agt tac ctc cct gtg 1907
 Arg Gln Val Val Phe Thr Ser Asp Pro His Lys Ser Tyr Leu Pro Val
 560 565 570 575

caa ttc cag tca cct gat aaa gca gaa gcc cag cgt gga gac ccg tct 1955
 Gln Phe Gln Ser Pro Asp Lys Ala Glu Ala Gln Arg Gly Asp Pro Ser
 580 585 590

gtt att tct gtc aat ggc act gac ttt acc ttc cga agt gca ggc gtc 2003
 Val Ile Ser Val Asn Gly Thr Asp Phe Thr Phe Arg Ser Ala Gly Val
 595 600 605

ctc ctc ctt gtt gtg gat ccg tgc agc gtt cca ttc cgc ttg acg gaa 2051
 Leu Leu Leu Val Val Asp Pro Cys Ser Val Pro Phe Arg Leu Thr Glu
 610 615 620

aaa acg gtt ttt cct ctt gct gat gtc agt cgc att gaa gag tat tta 2099
 Lys Thr Val Phe Pro Leu Ala Asp Val Ser Arg Ile Glu Glu Tyr Leu
 625 630 635

aaa aca ggc atc cct cca agg tcc att gtt ctg ttg agc aca aga gga 2147
 Lys Thr Gly Ile Pro Pro Arg Ser Ile Val Leu Leu Ser Thr Arg Gly
 640 645 650 655

gaa ata aag cag tta aac att tca cac tta cta gta cct ctg gga tta 2195
 Glu Ile Lys Gln Leu Asn Ile Ser His Leu Leu Val Pro Leu Gly Leu
 660 665 670

gcc aaa cca gct cat ctt tat gac aaa ggg agt acc gta ttt ttg gga 2243

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Ala Lys Pro Ala His Leu Tyr Asp Lys Gly Ser Thr Val Phe Leu Gly
675 680 685

ttc agt gga aac ttt aaa cca tca tgg act aag cta ttt acc agt cct 2291
Phe Ser Gly Asn Phe Lys Pro Ser Trp Thr Lys Leu Phe Thr Ser Pro
690 695 700

gct gga cag ggc ctt ggg gtg ctt gaa caa ttc ata cct ttg cag ctg 2339
Ala Gly Gln Gly Leu Gly Val Leu Glu Gln Phe Ile Pro Leu Gln Leu
705 710 715

gac gaa tat ggt tgt ccc aga gcc acc act gtc cgc aga aga gac ctg 2387
Asp Glu Tyr Gly Cys Pro Arg Ala Thr Thr Val Arg Arg Arg Asp Leu
720 725 730 735

gaa ctg cta aag caa gct tca aaa gca cat tagagactaa ctgtaactta 2437
Glu Leu Leu Lys Gln Ala Ser Lys Ala His
740 745

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gttgtttgta tttgtaaggc tgggtgtattc agagagcaga tctcttattc ctcactttcc 2677

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tgttcagcag tgccctggggc cctgtttctg ggcagccttt gaggattttc tatgatattg 2917

aatgacagtt ttaagtggca actcaggccc agtcatgcc cttttttgcc tggacatgtg 2977

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ctatTTTTat tcacttatat atcaattact tgtaagggtt aaactttcaa acaggaagta 3037
tattgggaca aaagggtctt tggggattag atatcccttt aatctgtgac cattgggcaa 3097
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tcattagagt gtgtgtgtgt gtgtgtgtgt gtgtgtgttt tatgacttaa atatctttac 4117

gtgtgttttt tagagcttgg ttcttttaaag atttggagaa gatatgtaaa ttaccaaggc 4177

acttggtttt tctgttttat atactaataa tcagggccta agttaataa aaatatgtgt 4237

gcatgtattt t 4248

<210> 6

<211> 745

<212> PRT

<213> Homo sapiens

<400> 6

Met	Cys	Thr	Thr	Met	Arg	Asp	Lys	Val	Phe	Gly	Asn	Tyr	Ile	Pro	Val
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Pro	Ala	Thr	Asp	Cys	Met	Ala	Val	Ser	Thr	Phe	Trp	Ile	Ala	His	Pro
		20					25						30		

Asn	Asn	Asn	Leu	Ile	Asn	Asn	Ala	Ala	Ala	Gly	Ser	Gln	Asp	Ala	Gly
		35					40						45		

Ile	Trp	Tyr	Leu	Phe	His	Lys	Glu	Pro	Thr	Gly	Glu	Ser	Ser	Gly	Leu
	50					55					60				

Gln	Leu	Leu	Ala	Lys	Pro	Glu	Leu	Thr	Pro	Leu	Gly	Ile	Phe	Tyr	Asn
65				70					75					80	

Asn	Arg	Val	His	Ser	Asn	Phe	Lys	Ala	Gly	Leu	Phe	Ile	Asp	Lys	Gly
			85						90					95	

Val	Lys	Thr	Thr	Asn	Ser	Ser	Ala	Ala	Asp	Pro	Arg	Glu	Tyr	Leu	Cys
		100						105						110	

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Leu Asp Asn Ser Ala Arg Phe Arg Pro His Gln Asp Ala Asn Pro Glu
115 120 125

Lys Pro Arg Val Ala Ala Leu Ile Asp Arg Leu Ile Ala Phe Lys Asn
130 135 140

Asn Asp Asn Gly Ala Trp Val Arg Gly Gly Asp Ile Ile Val Gln Asn
145 150 155 160

Ser Ala Phe Ala Asp Asn Gly Ile Gly Leu Thr Phe Ala Ser Asp Gly
165 170 175

Ser Phe Pro Ser Asp Glu Gly Ser Ser Gln Glu Val Ser Glu Ser Leu
180 185 190

Phe Val Gly Glu Ser Arg Asn Tyr Gly Phe Gln Gly Gly Gln Asn Lys
195 200 205

Tyr Val Gly Thr Gly Gly Ile Asp Gln Lys Pro Arg Thr Leu Pro Arg
210 215 220

Asn Arg Thr Phe Pro Ile Arg Gly Phe Gln Ile Tyr Asp Gly Pro Ile
225 230 235 240

His Leu Thr Arg Ser Thr Phe Lys Lys Tyr Val Pro Thr Pro Asp Arg
245 250 255

Tyr Ser Ser Ala Ile Gly Phe Leu Met Lys Asn Ser Trp Gln Ile Thr
260 265 270

Pro Arg Asn Asn Ile Ser Leu Val Lys Phe Gly Pro His Val Ser Leu
275 280 285

Asn Val Phe Phe Gly Lys Pro Gly Pro Trp Phe Glu Asp Cys Glu Met
290 295 300

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Asp Gly Asp Lys Asn Ser Ile Phe His Asp Ile Asp Gly Ser Val Thr
305 310 315 320

Gly Tyr Lys Asp Ala Tyr Val Gly Arg Met Asp Asn Tyr Leu Ile Arg
325 330 335

His Pro Ser Cys Val Asn Val Ser Lys Trp Asn Ala Val Ile Cys Ser
340 345 350

Gly Thr Tyr Ala Gln Val Tyr Val Gln Thr Trp Ser Thr Gln Asn Leu
355 360 365

Ser Met Thr Ile Thr Arg Asp Glu Tyr Pro Ser Asn Pro Met Val Leu
370 375 380

Arg Gly Ile Asn Gln Lys Ala Ala Phe Pro Gln Tyr Gln Pro Val Val
385 390 395 400

Met Leu Glu Lys Gly Tyr Thr Ile His Trp Asn Gly Pro Ala Pro Arg
405 410 415

Thr Thr Phe Leu Tyr Leu Val Asn Phe Asn Lys Asn Asp Trp Ile Arg
420 425 430

Val Gly Leu Cys Tyr Pro Ser Asn Thr Ser Phe Gln Val Thr Phe Gly
435 440 445

Tyr Leu Gln Arg Gln Asn Gly Ser Leu Ser Lys Ile Glu Glu Tyr Glu
450 455 460

Pro Val His Ser Leu Glu Glu Leu Gln Arg Lys Gln Ser Glu Arg Lys
465 470 475 480

Phe Tyr Phe Asp Ser Ser Thr Gly Leu Leu Phe Leu Tyr Leu Lys Ala
485 490 495

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Lys Ser His Arg His Gly His Ser Tyr Cys Ser Ser Gln Gly Cys Glu
500 505 510

Arg Val Lys Ile Gln Ala Ala Thr Asp Ser Lys Asp Ile Ser Asn Cys
515 520 525

Met Ala Lys Ala Tyr Pro Gln Tyr Tyr Arg Lys Pro Ser Val Val Lys
530 535 540

Arg Met Pro Ala Met Leu Thr Gly Leu Cys Gln Gly Cys Gly Thr Arg
545 550 555 560

Gln Val Val Phe Thr Ser Asp Pro His Lys Ser Tyr Leu Pro Val Gln
565 570 575

Phe Gln Ser Pro Asp Lys Ala Glu Ala Gln Arg Gly Asp Pro Ser Val
580 585 590

Ile Ser Val Asn Gly Thr Asp Phe Thr Phe Arg Ser Ala Gly Val Leu
595 600 605

Leu Leu Val Val Asp Pro Cys Ser Val Pro Phe Arg Leu Thr Glu Lys
610 615 620

Thr Val Phe Pro Leu Ala Asp Val Ser Arg Ile Glu Glu Tyr Leu Lys
625 630 635 640

Thr Gly Ile Pro Pro Arg Ser Ile Val Leu Leu Ser Thr Arg Gly Glu
645 650 655

Ile Lys Gln Leu Asn Ile Ser His Leu Leu Val Pro Leu Gly Leu Ala
660 665 670

Lys Pro Ala His Leu Tyr Asp Lys Gly Ser Thr Val Phe Leu Gly Phe
675 680 685

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Ser Gly Asn Phe Lys Pro Ser Trp Thr Lys Leu Phe Thr Ser Pro Ala
 690 695 700

Gly Gln Gly Leu Gly Val Leu Glu Gln Phe Ile Pro Leu Gln Leu Asp
 705 710 715 720

Glu Tyr Gly Cys Pro Arg Ala Thr Thr Val Arg Arg Arg Asp Leu Glu
 725 730 735

Leu Leu Lys Gln Ala Ser Lys Ala His
 740 745

<210> 7

<211> 1545

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (341)..(1006)

<400> 7

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tgcttagctc tcctctcaat attcaaactc ctagaacacgtt gttgttttgt ctttcccatg 120

gacacggctc ccaggcctct gacccttgcct ctaattggga cctgctgtgt ggccctccct 180

tgcttaccag ctgacaggaa cccttctctc cccccaggtt ggacacgccg tttccaaggc 240

ctcatggctt cctttttctt gggttactgcc tcgggtctcc tgggagagat ctcttttggtg 300

ccgaaaaccg gaacgggaag cctcagcacc ctggcccccc atg ccc ctc gtg ggg 355

Met Pro Leu Val Gly

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[illegible]

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135	140	145	
cgg ccc cgc cct cac tca tcc tgc aga ggg cac tgg gcc agt ggc cga			835
Arg Pro Arg Pro His Ser Ser Cys Arg Gly His Trp Ala Ser Gly Arg			
150	155	160	165
cat ggt ggg ttg gat ggg cat gac tgc agt ggc aaa gcc tgg tcg gcc			883
His Gly Gly Leu Asp Gly His Asp Cys Ser Gly Lys Ala Trp Ser Ala			
	170	175	180
ttt cag acg gct ctg atc cca ttc ccg aac ctg ggc tgc act tca gga			931
Phe Gln Thr Ala Leu Ile Pro Phe Pro Asn Leu Gly Cys Thr Ser Gly			
	185	190	195
gcg gaa gcc agc ctg acg tgc ttt ctg tcc ctt tcc aga gtc aca aat			979
Ala Glu Ala Ser Leu Thr Cys Phe Leu Ser Leu Ser Arg Val Thr Asn			
	200	205	210
gag agg gtc cac agc ggt gtc ctc ctc tgaccacgcc gcccccttca			1026
Glu Arg Val His Ser Gly Val Leu Leu			
	215	220	
agcgaccaca ctccaccatc tcagacagca gcacctctc ttctagcagc cagtcctcct			1086
ccatcctggg gtcgctgggc ctgcttgtgt cctccagccc agcccaccg ggcctatgga			1146
gccctgcccc cagccccctgg tcatttgata tcagagcctg cgtcgaggaa gatgagccag			1206
agccagaact agagacgggc acccaggtg cagtgtgtga gggggctcct gctgtgctgc			1266
tgagccgcac acgccaggcc tgatgactgt cagggtggca gtgcccatca tgtggctaga			1326
acaatacaga gggagcagca cgccaggcct gatgactctg ggggtggcgg tgcccatcgc			1386
gtggctggaa cgatccagag ggaatagcac agcagggtgc caggattttc ccaggatttt			1446

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agacattccc taacattttc aaacaaattt acaattttgt cttattttaaa aaacaaacct 1506

tccacttcca cccaagacaa cagcatagga aacagacct 1545

<210> 8

<211> 222

<212> PRT

<213> Homo sapiens

<400> 8

Met Pro Leu Val Gly Gln Gly Gly Tyr Thr Leu Tyr Thr Leu Leu Val
1 5 10 15

Trp Ala Glu Gly Ile Arg Gly Thr Gly Arg Leu Trp Gly Gly Ile Ser
20 25 30

Pro Arg Val Ala Leu Glu Thr Val Ile Leu Ser Ser Val Leu Glu Leu
35 40 45

Arg Ile Gln Glu Met Ala Ser Met Gly Ile Gly Asn Gln Pro Phe Met
50 55 60

Asp Val Lys Pro Arg Asp Arg Thr Pro Asp Cys Ala Val Ile Ser Asp
65 70 75 80

Gly Ala Pro Lys Cys Ala Val Met Ser Asp Arg Val Pro Asp Ser Ile
85 90 95

Val Lys Gly Thr Gly Thr Val Ala Arg Ser Arg Pro His Ser Pro Cys
100 105 110

Arg Gly His Trp Ala Cys His Gln Gly His Gly Tyr Gly Gly Ile Gly
115 120 125

Pro Thr Leu Thr Arg Pro Gln Ser Ala Pro Gly Leu Ser Ser Arg Thr

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130	135	140
Arg Val Arg Trp Pro Arg Pro Arg Pro His Ser Ser Cys Arg Gly His		
145	150	155
Trp Ala Ser Gly Arg His Gly Gly Leu Asp Gly His Asp Cys Ser Gly		
	165	170
		175
Lys Ala Trp Ser Ala Phe Gln Thr Ala Leu Ile Pro Phe Pro Asn Leu		
	180	185
		190
Gly Cys Thr Ser Gly Ala Glu Ala Ser Leu Thr Cys Phe Leu Ser Leu		
	195	200
		205
Ser Arg Val Thr Asn Glu Arg Val His Ser Gly Val Leu Leu		
	210	215
		220

<210> 9

<211> 30

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially
synthesized oligo-cap linker sequence

<400> 9

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30

<210> 10

<211> 42

<212> DNA

<213> Artificial Sequence

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<220>

<223> Description of Artificial Sequence:an artificially
synthesized oligo(dT) primer sequence

<400> 10

gcggctgaag acggcctatg tggccttttt tttttttttt tt

42

<210> 11

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

<400> 11

agcatcgagt cggccttggtt g

21

<210> 12

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

<400> 12

gcggctgaag acggcctatg t

21